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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : C12N 1/21, 5/10, 9/48, 9/50, 9/64, 15/55, 15/63 — A1

(11) International Publication Number: WO 99/09138

(43) International Publication Date: 25 February 1999 (25.02.99)

(21) International Application Number: PCT/US98/17372

(22) International Filing Date: 21 August 1998 (21.08.98)

(30) Priority Data:
08/915,659 21 August 1997 (21.08.97) US

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(81) Designated States: AU, CA, JP, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).

Published
With international search report.

(54) Title: NOVEL EXTRACELLULAR SERINE PROTEASE

(57) Abstract

The present invention provides a DNA encoding a TADG-14 protein selected from the group consisting of: (a) isolated DNA which encodes a TADG-14 protein; (b) isolated DNA which hybridizes to isolated DNA of (a) above and which encodes a TADG-14 protein; and (c) isolated DNA differing from the isolated DNAs of (a) and (b) above in codon sequence due to the degeneracy of the genetic code, and which encodes a TADG-14 protein. Also provided is a vector capable of expressing the DNA of the present invention adapted for expression in a recombinant cell and regulatory elements necessary for expression of the DNA in the cell.

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NOVEL EXTRACELLULAR SERINE PROTEASE

BACKGROUND OF THE INVENTION

Field of the Invention

The present invention relates generally to the fields of cellular biology and the diagnosis of neoplastic disease. More specifically, this invention relates to a novel extracellular serine protease termed Tumor Antigen Derived Gene-14 (TADG-14).

Description of the Related Art

Extracellular proteases have been directly associated with tumor growth, shedding of tumor cells and invasion of target organs. Individual classes of proteases are involved in, but not limited to (1) the digestion of stroma surrounding the initial tumor area, (2) the digestion of the cellular adhesion molecules to allow dissociation of tumor cells; and (3) the invasion of the basement membrane for metastatic growth and the activation of both tumor growth factors and angiogenic factors.

The prior art is deficient in the lack of effective means of screening to identify proteases overexpressed in carcinoma. The present invention fulfills this longstanding need in the art.

SUMMARY OF THE INVENTION

The present invention discloses a screening system to identify proteases overexpressed in carcinoma by examining PCR products amplified from early-stage tumors, metastatic tumors, and normal ovarian epithelium.

In one embodiment of the present invention, there is provided a DNA encoding a TADG-14 protein selected from the group consisting of: (a) isolated DNA which encodes a TADG-14 protein; (b) isolated DNA which hybridizes to isolated DNA of (a) above and which encodes a TADG-14 protein; and (c) isolated DNA differing from the isolated DNAs of (a) and (b) above in codon sequence due to the degeneracy of the genetic code, and which encodes a TADG-14 protein.

In another embodiment of the present invention, there is provided a vector capable of expressing the DNA of the present invention adapted for expression in a recombinant cell and regulatory elements necessary for expression of the DNA in the cell.

In yet another embodiment of the present invention, there is provided a host cell transfected with the vector of the present invention, said vector expressing a TADG-14 protein

In still yet another embodiment of the present invention, there is provided a method of detecting expression of a TADG-14 mRNA, comprising the steps of: (a) contacting mRNA

obtained from the cell with the labeled hybridization probe; and (b) detecting hybridization of the probe with the mRNA.

Other and further aspects, features, and advantages of the present invention will be apparent from the following description of the presently preferred embodiments of the invention given for the purpose of disclosure.

BRIEF DESCRIPTION OF THE DRAWINGS

So that the matter in which the above-recited features, advantages and objects of the invention, as well as others which will become clear, are attained and can be understood in detail, more particular descriptions of the invention briefly summarized above may be had by reference to certain embodiments thereof which are illustrated in the appended drawings. These drawings form a part of the specification. It is to be noted, however, that the appended drawings illustrate preferred embodiments of the invention and therefore are not to be considered limiting in their scope.

Figure 1 shows a comparison of PCR products derived from normal and carcinoma cDNA as shown by staining in an agarose gel. Two distinct bands (lane 2) were present in the primer pair sense-His-antisense Asp (AS1) and multiple bands of about 500 base pairs are noted in the carcinoma lane for the sense-His antisense-Ser (AS2) primer pairs (lane 4).

Figure 2 shows a comparison of the amino acid sequence of TADG-14's catalytic domains.

Figure 3 shows the overexpression of TADG-14 in ovarian carcinomas.

Figure 4 shows the TADG-14 expression in tumors and cell lines.

Figure 5 shows the blots of TADG-14 expression in fetal, adult and ovarian carcinoma tissues.

Figure 6 shows the complete sequence of the TADG-14 transcript including the open reading frame and common domains.

Figure 7 shows the homology of TADG-14 with mouse neuropsin. There was approximately 76% identity for the open reading frame and low homology outside of the open reading frame.

Figure 8 shows the amino acid homology of TADG-14 with mouse neuropsin.

Figure 9 shows the Northern Blot analysis. (Figure 9A) Messenger RNA was isolated from the tissues of interest and subjected to Northern hybridization using a random labeled 230 bp TADG14 specific RT-PCR product. The blot was stripped and probed for β-tubulin. (Figure 9B, Figure 9C, Figure 9D) Multiple tissue Northern blots (Clontech) were probed with the same TADG14 and β-tubulin specific RT-PCR products. TADG14 mRNA was detected as a 1.4-kb transcript in tumors and was not detected in any normal tissue studied.

Figure 10 shows the cDNA and deduced amino acid sequences of TADG14 and comparison of predicted TADG14 sequence with known proteases. The cDNA sequence of TADG14 is shown with its deduced 260 amino acid sequence represented by the one-letter code for each residue. Within the cDNA, the underlined portions represent the Kozak's consensus sequence for initiation of translation and the polyadenylation signal, respectively. The TADG14 protein sequence contains a secretion

signal sequence near its amino terminus (shaded green). The critical residues of the catalytic triad are identified by yellow shading while a potential glycosylation site is marked with purple shading. The stop codon is represented by the (*) symbol. Using the GCG PILEUP program (REF), the amino acid sequence of TADG14 was compared to human glandular kallikrein (hHk2, accession # P06870), human PSA (hPSA, accession # P07288), mouse neuropsin (mNeur, accession # D30785) and human Protease M (hProM, accession # U62801). Amino acid residues that are identical in at least three of the five sequences are shaded in green. Those residues shaded in yellow represent amino acids that are similar among at least three sequences. The positions of the residues of the catalytic triad are marked.

Figure 11 shows the TADG14 quantitative PCR. Typical results of a TADG14 quantitative PCR experiment are shown (Figure 11A). The reaction products were electrophoresed through a 2% agarose TAE gel and stained with ethidium bromide. In this figure, the 454-bp band represents the β-tubulin product and the 230-bp band represents the TADG14 product. The radiolabeled PCR products were quantitated. (Figure 11B) As determined by the student's t test, TADG14 mRNA expression levels were significantly elevated in LMP tumors (*, $P=0.05$) and carcinomas ($P<0.0001$) compared to levels found in normal ovary. Individual cases are represented in a scatter plot. This is indicative of heterogeneity of TADG14 expression among these tumor samples.

Figure 12 shows a Western Blot. Polyclonal antibodies were generated by immunization of rabbits with one of three poly-lysine linked multiple antigen peptides derived from the deduced

amino acid sequence of TADG14. These sequences are KYTVRLGDHSLQ (T14-1), GHECQPHSQPWQ (T14-2), and LDWIKKIIGSKG (T14-3). (A) For Western blot analysis, approximately 20 g of MDA-MB-435S and HeLa cell lysates were separated on a 15% SDS-PAGE gel and electroblotted to PVDF at 100V for 40 minutes at 4 C. The blot was blocked overnight in Tris-buffered saline (TBS), pH 7.8 containing 0.2% non-fat milk. Primary antibody was added to the membrane at a dilution of 1:100 in 0.2% milk/TBS and incubated for 2 hours at room temperature. The blot was washed and incubated with 1:3000 dilution of alkaline-phosphatase conjugated goat and anti-rabbit IgG antibody (Bio-Rad) for one hour at room temperature. The blot was washed and incubated with a chemiluminescent substrate (Bio-Rad) before a 10-second exposure to X-ray film for visualization.

Figure 13 shows immunohistochemistry. Staining was with the TADG14-1 antibody for normal ovary, two serous carcinomas, mucinous carcinoma, endometrioid carcinoma and clear cell carcinoma of the ovary (A, B, C, D, E and F, respectively). No staining was observed in normal ovary. The serous carcinoma shown in figure B has TADG14 most strongly associated with the surface of the tumor, while in the serous tumor in figure C, TADG14 is found in a granular form in an apparent secretion pathway. In mucinous carcinoma TADG14 appears to be most highly expressed along the invasive front of the tumor. TADG14 is secreted into the lumen of the glandular structure formed by the endometrioid carcinoma in figure E. The clear cell carcinoma stained in panel F shows diffuse staining throughout all tumor cells.

DETAILED DESCRIPTION OF THE INVENTION

As used herein, the term "cDNA" shall refer to the DNA copy of the mRNA transcript of a gene.

As used herein, the term "derived amino acid sequence" shall mean the amino acid sequence determined by reading the triplet sequence of nucleotide bases in the cDNA.

As used herein the term "screening a library" shall refer to the process of using a labeled probe to check whether, under the appropriate conditions, there is a sequence complementary to the probe present in a particular DNA library. In addition, "screening a library" could be performed by PCR.

As used herein, the term "PCR" refers to the polymerase chain reaction that is the subject of U.S. Patent Nos. 4,683,195 and 4,683,202 to Mullis, as well as other improvements now known in the art.

The TADG-14 cDNA is 1343 base pairs long (SEQ IS No: 6) and encoding for a 260 amino acid protein (SEQ IS No: 7). The availability of the TADG-14 gene opens the way for a number studies that can lead to various applications. For example, the TADG-14 gene underlies a specific human genetic disease, the cDNA can be the basis for a diagnostic predictive test.

In accordance with the present invention there may be employed conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, e.g., Maniatis, Fritsch & Sambrook, "Molecular Cloning: A Laboratory Manual (1982); "DNA Cloning: A Practical Approach," Volumes I and II (D.N.

Glover ed. 1985); "Oligonucleotide Synthesis" (M.J. Gait ed. 1984); "Nucleic Acid Hybridization" [B.D. Hames & S.J. Higgins eds. (1985)]; "Transcription and Translation" [B.D. Hames & S.J. Higgins eds. (1984)]; "Animal Cell Culture" [R.I. Freshney, ed. (1986)]; "Immobilized Cells And Enzymes" [IRL Press, (1986)]; B. Perbal, "A Practical Guide To Molecular Cloning" (1984).

Therefore, if appearing herein, the following terms shall have the definitions set out below.

The amino acid described herein are preferred to be in the "L" isomeric form. However, residues in the "D" isomeric form can be substituted for any L-amino acid residue, as long as the desired functional property of immunoglobulin-binding is retained by the polypeptide. NH_2 refers to the free amino group present at the amino terminus of a polypeptide. COOH refers to the free carboxy group present at the carboxy terminus of a polypeptide. In keeping with standard polypeptide nomeclature, *J Biol. Chem.*, 243:3552-59 (1969), abbreviations for amino acids may be used.

It should be noted that all amino-acid residue sequences are represented herein by formulae whose left and right orientation is in the conventional direction of amino-terminus to carboxy-terminus. Furthermore, it should be noted that a dash at the beginning or end of an amino acid residue sequence indicates a peptide bond to a further sequence of one or more amino-acid residues. The above Table is presented to correlate the three-letter and one-letter notations which may appear alternately herein.

A "replicon" is any genetic element (e.g., plasmid, chromosome, virus) that functions as an autonomous unit of DNA replication *in vivo*; i.e., capable of replication under its own control.

A "vector" is a replicon, such as plasmid, phage or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

A "DNA molecule" refers to the polymeric form of deoxyribonucleotides (adenine, guanine, thymine, or cytosine) in its either single stranded form, or a double-stranded helix. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, *inter alia*, in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes. In discussing the structure herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the nontranscribed strand of DNA (i.e., the strand having a sequence homologous to the mRNA).

An "origin of replication" refers to those DNA sequences that participate in DNA synthesis.

A DNA "coding sequence" is a double-stranded DNA sequence which is transcribed and translated into a polypeptide *in vivo* when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxyl) terminus. A coding sequence can include, but is not limited to, prokaryotic sequences, cDNA from eukaryotic mRNA, genomic DNA sequences from eukaryotic (e.g., mammalian) DNA, and even synthetic DNA sequences. A polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence.

Transcriptional and translational control sequences are DNA regulatory sequences, such as promoters, enhancers,

polyadenylation signals, terminators, and the like, that provide for the expression of a coding sequence in a host cell.

A "promoter sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bounded at its 3' terminus by the transcription initiation site and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site, as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase. Eukaryotic promoters often, but not always, contain "TATA" boxes and "CAT" boxes. Prokaryotic promoters contain Shine-Dalgarno sequences in addition to the -10 and -35 consensus sequences.

An "expression control sequence" is a DNA sequence that controls and regulates the transcription and translation of another DNA sequence. A coding sequence is "under the control" of transcriptional and translational control sequences in a cell when RNA polymerase transcribes the coding sequence into mRNA, which is then translated into the protein encoded by the coding sequence.

A "signal sequence" can be included near the coding sequence. This sequence encodes a signal peptide, N-terminal to the polypeptide, that communicates to the host cell to direct the polypeptide to the cell surface or secrete the polypeptide into the media, and this signal peptide is clipped off by the host cell before the protein leaves the cell. Signal sequences can be found

associated with a variety of proteins native to prokaryotes and eukaryotes.

The term "oligonucleotide", as used herein in referring to the probe of the present invention, is defined as a molecule comprised of two or more ribonucleotides, preferably more than three. Its exact size will depend upon many factors which, in turn, depend upon the ultimate function and use of the oligonucleotide.

The term "primer" as used herein refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product, which is complementary to a nucleic acid strand, is induced, i.e., in the presence of nucleotides and an inducing agent such as a DNA polymerase and at a suitable temperature and pH. The primer may be either single-stranded or double-stranded and must be sufficiently long to prime the synthesis of the desired extension product in the presence of the inducing agent. The exact length of the primer will depend upon many factors, including temperature, source of primer and use the method. For example, for diagnostic applications, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 15-25 or more nucleotides, although it may contain fewer nucleotides.

The primers herein are selected to be "substantially" complementary to different strands of a particular target DNA sequence. This means that the primers must be sufficiently complementary to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the template. For example, a non-complementary nucleotide

fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence or hybridize therewith and thereby form the template for the synthesis of the extension product.

As used herein, the terms "restriction endonucleases" and "restriction enzymes" refer to enzymes, each of which cut double-stranded DNA at or near a specific nucleotide sequence.

A cell has been "transformed" by exogenous or heterologous DNA when such DNA has been introduced inside the cell. The transforming DNA may or may not be integrated (covalently linked) into the genome of the cell. In prokaryotes, yeast, and mammalian cells for example, the transforming DNA may be maintained on an episomal element such as a plasmid. With respect to eukaryotic cells, a stably transformed cell is one in which the transforming DNA has become integrated into a chromosome so that it is inherited by daughter cells through chromosome replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cells containing the transforming DNA. A "clone" is a population of cells derived from a single cell or ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of stable growth *in vitro* for many generations.

Two DNA sequences are "substantially homologous" when at least about 75% (preferably at least about 80%, and most preferably at least about 90% or 95%) of the nucleotides match

over the defined length of the DNA sequences. Sequences that are substantially homologous can be identified by comparing the sequences using standard software available in sequence data banks, or in a Southern hybridization experiment under, for example, stringent conditions as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. See, e.g., Maniatis et al., *supra*; DNA Cloning, Vols. I & II, *supra*; Nucleic Acid Hybridization, *supra*.

A "heterologous' region of the DNA construct is an identifiable segment of DNA within a larger DNA molecule that is not found in association with the larger molecule in nature. Thus, when the heterologous region encodes a mammalian gene, the gene will usually be flanked by DNA that does not flank the mammalian genomic DNA in the genome of the source organism. In another example, coding sequence is a construct where the coding sequence itself is not found in nature (e.g., a cDNA where the genomic coding sequence contains introns, or synthetic sequences having codons different than the native gene). Allelic variations or naturally-occurring mutational events do not give rise to a heterologous region of DNA as defined herein.

The labels most commonly employed for these studies are radioactive elements, enzymes, chemicals which fluoresce when exposed to untraviolet light, and others. A number of fluorescent materials are known and can be utilized as labels. These include, for example, fluorescein, rhodamine, auramine, Texas Red, AMCA blue and Lucifer Yellow. A particular detecting material is anti-rabbit antibody prepared in goats and conjugated with fluorescein through an isothiocyanate.

Proteins can also be labeled with a radioactive element or with an enzyme. The radioactive label can be detected by any of the currently available counting procedures. The preferred isotope may be selected from ^{3}H, ^{14}C, ^{32}P, ^{35}S, ^{36}Cl, ^{51}Cr, ^{57}Co, ^{58}Co, ^{59}Fe, ^{90}Y, ^{125}I, ^{131}I, and ^{186}Re.

Enzyme labels are likewise useful, and can be detected by any of the presently utilized colorimetric, spectrophotometric, fluorospectrophotometric, amperometric or gasometric techniques. The enzyme is conjugated to the selected particle by reaction with bridging molecules such as carbodiimides, diisocyanates, glutaraldehyde and the like. Many enzymes which can be used in these procedures are known and can be utilized. The preferred are peroxidase, β-glucuronidase, β-D-glucosidase, β-D-galactosidase, urease, glucose oxidase plus peroxidase and alkaline phosphatase. U.S. Patent Nos. 3,654,090, 3,850,752, and 4,016,043 are referred to by way of example for their disclosure of alternate labeling material and methods.

A particular assay system developed and utilized in the art is known as a receptor assay. In a receptor assay, the material to be assayed is appropriately labeled and then certain cellular test colonies are inoculated with a quantitiy of both the label after which binding studies are conducted to determine the extent to which the labeled material binds to the cell receptors. In this way, differences in affinity between materials can be ascertained.

An assay useful in the art is known as a "cis/trans" assay. Briefly, this assay employs two genetic constructs, one of which is typically a plasmid that continually expresses a particular receptor of interest when transfected into an appropriate cell line, and the second of which is a plasmid that expresses a reporter

such as luciferase, under the control of a receptor/ligand complex. Thus, for example, if it is desired to evaluate a compound as a ligand for a particular receptor, one of the plasmids would be a construct that results in expression of the receptor in the chosen cell line, while the second plasmid would possess a promoter linked to the luciferase gene in which the response element to the particular receptor is inserted. If the compound under test is an agonist for the receptor, the ligand will complex with the receptor, and the resulting complex will bind the response element and initiate transcription of the luciferase gene. The resulting chemiluminescence is then measured photometrically, and dose response curves are obtained and compared to those of known ligands. The foregoing protocol is described in detail in U.S. Patent No. 4,981,784.

As used herein, the term "host" is meant to include not only prokaryotes but also eukaryotes such as yeast, plant and animal cells. A recombinant DNA molecule or gene which encodes a human TADG-14 protein of the present invention can be used to transform a host using any of the techniques commonly known to those of ordinary skill in the art. Especially preferred is the use of a vector containing coding sequences for the gene which encodes a human TADG-14 protein of the present invention for purposes of prokaryote transformation.

Prokaryotic hosts may include *E. coli*, *S. tymphimurium*, *Serratia marcescens* and *Bacillus subtilis*. Eukaryotic hosts include yeasts such as *Pichia pastoris*, mammalian cells and insect cells.

In general, expression vectors containing promoter sequences which facilitate the efficient transcription of the inserted DNA fragment are used in connection with the host. The

expression vector typically contains an origin of replication, promoter(s), terminator(s), as well as specific genes which are capable of providing phenotypic selection in transformed cells. The transformed hosts can be fermented and cultured according to means known in the art to achieve optimal cell growth.

The invention includes a substantially pure DNA encoding a TADG-14 protein, a strand of which DNA will hybridize at high stringency to a probe containing a sequence of at least 15 consecutive nucleotides of (SEQ ID NO:6). The protein encoded by the DNA of this invention may share at least 80% sequence identity (preferably 85%, more preferably 90%, and most preferably 95%) with the amino acids listed in Figure 6 (SEQ ID NO: 7). More preferably, the DNA includes the coding sequence of the nucleotides of Figure 6 (SEQ ID NO:6), or a degenerate variant of such a sequence.

The probe to which the DNA of the invention hybridizes preferably consists of a sequence of at least 20 consecutive nucleotides, more preferably 40 nucleotides, even more preferably 50 nucleotides, and most preferably 100 nucleotides or more (up to 100%) of the coding sequence of the nucleotides listed in Figure 6 (SEQ ID NO: 6) or the complement thereof. Such a probe is useful for detecting expression of TADG-14 in a human cell by a method including the steps of (a) contacting mRNA obtained from the cell with the labeled hybridization probe; and (b) detecting hybridization of the probe with the mRNA.

This invention also includes a substantially pure DNA containing a sequence of at least 15 consecutive nucleotides (preferably 20, more preferably 30, even more preferably 50, and

most preferably all) of the region from nucleotides 1 to 1343 of the nucleotides listed in Figure 6 (SEQ ID NO: 6).

By "high stringency" is meant DNA hybridization and wash conditions characterized by high temperature and low salt concentration, e.g., wash conditions of 65°C at a salt concentration of approximately 0.1 x SSC, or the functional equivalent thereof. For example, high stringency conditions may include hybridization at about 42°C in the presence of about 50% formamide; a first wash at about 65°C with about 2 x SSC containing 1% SDS; followed by a second wash at about 65°C with about 0.1 x SSC.

By "substantially pure DNA" is meant DNA that is not part of a milieu in which the DNA naturally occurs, by virtue of separation (partial or total purification) of some or all of the molecules of that milieu, or by virtue of alteration of sequences that flank the claimed DNA. The term therefore includes, for example, a recombinant DNA which is incorporated into a vector, into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote; or which exists as a separate molecule (e.g., a cDNA or a genomic or cDNA fragment produced by polymerase chain reaction (PCR) or restriction endonuclease digestion) independent of other sequences. It also includes a recombinant DNA which is part of a hybrid gene encoding additional polypeptide sequence, e.g., a fusion protein. Also included is a recombinant DNA which includes a portion of the nucleotides listed in Figure 6 (SEQ ID NO: 6) which encodes an alternative splice variant of TADG-14.

The DNA may have at least about 70% sequence identity to the coding sequence of the nucleotides listed in Figure 6 (SEQ ID NO:6), preferably at least 75% (e.g. at least 80%); and

most preferably at least 90%. The identity between two sequences is a direct function of the number of matching or identical positions. When a subunit position in both of the two sequences is occupied by the same monomeric subunit, e.g., if a given position is occupied by an adenine in each of two DNA molecules, then they are identical at that position. For example, if 7 positions in a sequence 10 nucleotides in length are identical to the corresponding positions in a second 10-nucleotide sequence, then the two sequences have 70% sequence identity. The length of comparison sequences will generally be at least 50 nucleotides, preferably at least 60 nucleotides, more preferably at least 75 nucleotides, and most preferably 100 nucleotides. Sequence identity is typically measured using sequence analysis software (e.g., Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705).

The present invention comprises a vector comprising a DNA sequence coding for a which encodes a human TADG-14 protein and said vector is capable of replication in a host which comprises, in operable linkage: a) an origin of replication; b) a promoter; and c) a DNA sequence coding for said protein. Preferably, the vector of the present invention contains a portion of the DNA sequence shown in SEQ ID No: 6. A "vector" may be defined as a replicable nucleic acid construct, e.g., a plasmid or viral nucleic acid. Vectors may be used to amplify and/or express nucleic acid encoding TADG-14 protein. An expression vector is a replicable construct in which a nucleic acid sequence encoding a polypeptide is operably linked to suitable control sequences capable of effecting expression of the polypeptide in a cell. The

need for such control sequences will vary depending upon the cell selected and the transformation method chosen. Generally, control sequences include a transcriptional promoter and/or enhancer, suitable mRNA ribosomal binding sites, and sequences which control the termination of transcription and translation. Methods which are well known to those skilled in the art can be used to construct expression vectors containing appropriate transcriptional and translational control signals. See for example, the techniques described in Sambrook et al., 1989, *Molecular Cloning: A Laboratory Manual* (2nd Ed.), Cold Spring Harbor Press, N.Y. A gene and its transcription control sequences are defined as being "operably linked" if the transcription control sequences effectively control the transcription of the gene. Vectors of the invention include, but are not limited to, plasmid vectors and viral vectors. Preferred viral vectors of the invention are those derived from retroviruses, adenovirus, adeno-associated virus, SV40 virus, or herpes viruses.

By a "substantially pure protein" is meant a protein which has been separated from at least some of those components which naturally accompany it. Typically, the protein is substantially pure when it is at least 60%, by weight, free from the proteins and other naturally-occurring organic molecules with which it is naturally associated in vivo. Preferably, the purity of the preparation is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight. A substantially pure TADG-14 protein may be obtained, for example, by extraction from a natural source; by expression of a recombinant nucleic acid encoding an TADG-14 polypeptide; or by chemically synthesizing the protein. Purity can be measured by any appropriate method,

e.g., column chromatography such as immunoaffinity chromatography using an antibody specific for TADG-14, polyacrylamide gel electrophoresis, or HPLC analysis. A protein is substantially free of naturally associated components when it is separated from at least some of those contaminants which accompany it in its natural state. Thus, a protein which is chemically synthesized or produced in a cellular system different from the cell from which it naturally originates will be, by definition, substantially free from its naturally associated components. Accordingly, substantially pure proteins include eukaryotic proteins synthesized in *E. coli*, other prokaryotes, or any other organism in which they do not naturally occur.

In addition to substantially full-length proteins, the invention also includes fragments (e.g., antigenic fragments) of the TADG-14 protein (SEQ ID No: 7). As used herein, "fragment," as applied to a polypeptide, will ordinarily be at least 10 residues, more typically at least 20 residues, and preferably at least 30 (e.g., 50) residues in length, but less than the entire, intact sequence. Fragments of the TADG-14 protein can be generated by methods known to those skilled in the art, e.g., by enzymatic digestion of naturally occurring or recombinant TADG-14 protein, by recombinant DNA techniques using an expression vector that encodes a defined fragment of TADG-14, or by chemical synthesis. The ability of a candidate fragment to exhibit a characteristic of TADG-14 (e.g., binding to an antibody specific for TADG-14) can be assessed by methods described herein. Purified TADG-14 or antigenic fragments of TADG-14 can be used to generate new antibodies or to test existing antibodies (e.g., as positive controls in a diagnostic assay) by employing standard protocols known to

those skilled in the art. Included in this invention are polyclonal antisera generated by using TADG-14 or a fragment of TADG-14 as the immunogen in, e.g., rabbits. Standard protocols for monoclonal and polyclonal antibody production known to those skilled in this art are employed. The monoclonal antibodies generated by this procedure can be screened for the ability to identify recombinant TADG-14 cDNA clones, and to distinguish them from known cDNA clones.

Further included in this invention are TADG-14 proteins which are encoded at least in part by portions of SEQ ID NO: 7, e.g., products of alternative mRNA splicing or alternative protein processing events, or in which a section of TADG-14 sequence has been deleted. The fragment, or the intact TADG-14 polypeptide, may be covalently linked to another polypeptide, e.g. which acts as a label, a ligand or a means to increase antigenicity.

The invention also includes a polyclonal or monoclonal antibody which specifically binds to TADG-14. The invention encompasses not only an intact monoclonal antibody, but also an immunologically-active antibody fragment, e.g., a Fab or $(Fab)_2$ fragment; an engineered single chain Fv molecule; or a chimeric molecule, e.g., an antibody which contains the binding specificity of one antibody, e.g., of murine origin, and the remaining portions of another antibody, e.g., of human origin.

In one embodiment, the antibody, or a fragment thereof, may be linked to a toxin or to a detectable label, e.g. a radioactive label, non-radioactive isotopic label, fluorescent label, chemiluminescent label, paramagnetic label, enzyme label, or colorimetric label. Examples of suitable toxins include diphtheria toxin, *Pseudomonas* exotoxin A, ricin, and cholera toxin. Examples

of suitable enzyme labels include malate hydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, alcohol dehydrogenase, alpha-glycerol phosphate dehydrogenase, triose phosphate isomerase, peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase, acetylcholinesterase, etc. Examples of suitable radioisotopic labels include ^{3}H, ^{125}I, ^{131}I, ^{32}P, ^{35}S, ^{14}C, etc.

Paramagnetic isotopes for purposes of *in vivo* diagnosis can also be used according to the methods of this invention. There are numerous examples of elements that are useful in magnetic resonance imaging. For discussions on *in vivo* nuclear magnetic resonance imaging, see, for example, Schaefer et al., (1989) *JACC* 14, 472-480; Shreve et al., (1986) *Magn. Reson. Med.* 3, 336-340; Wolf, G. L., (1984) *Physiol. Chem. Phys. Med. NMR* 16, 93-95; Wesbey et al., (1984) *Physiol. Chem. Phys. Med. NMR* 16, 145-155; Runge et al., (1984) *Invest. Radiol.* 19, 408-415. Examples of suitable fluorescent labels include a fluorescein label, an isothiocyalate label, a rhodamine label, a phycoerythrin label, a phycocyanin label, an allophycocyanin label, an ophthaldehyde label, a fluorescamine label, etc. Examples of chemiluminescent labels include a luminal label, an isoluminal label, an aromatic acridinium ester label, an imidazole label, an acridinium salt label, an oxalate ester label, a luciferin label, a luciferase label, an aequorin label, etc.

Those of ordinary skill in the art will know of other suitable labels which may be employed in accordance with the present invention. The binding of these labels to antibodies or fragments thereof can be accomplished using standard techniques

commonly known to those of ordinary skill in the art. Typical techniques are described by Kennedy et al., (1976) *Clin. Chim. Acta* 70, 1-31; and Schurs et al., (1977) *Clin. Chim. Acta* 81, 1-40. Coupling techniques mentioned in the latter are the glutaraldehyde method, the periodate method, the dimaleimide method, the m-maleimidobenzyl-N-hydroxy-succinimide ester method.

Also within the invention is a method of detecting TADG-14 protein in a biological sample, which includes the steps of contacting the sample with the labelled antibody, e.g., radioactively tagged antibody specific for TADG-14, and determining whether the antibody binds to a component of the sample.

As described herein, the invention provides a number of diagnostic advantages and uses. For example, the TADG-14 protein is useful in diagnosing cancer in different tissues since this protein is absent in highly proliferating cells. Antibodies (or antigen-binding fragments thereof) which bind to an epitope specific for TADG-14, are useful in a method of detecting TADG-14 protein in a biological sample for diagnosis of cancerous or neoplastic transformation. This method includes the steps of obtaining a biological sample (e.g., cells, blood, tissue, etc.) from a patient suspected of having cancer, contacting the sample with a labelled antibody (e.g., radioactively tagged antibody) specific for TADG-14, and detecting the TADG-14 protein using standard immunoassay techniques such as an ELISA. Antibody binding to the biological sample indicates that the sample contains a component which specifically binds to an epitope within TADG-14.

Likewise, a standard Northern blot assay can be used to ascertain the relative amounts of TADG-14 mRNA in a cell or tissue obtained from a patient suspected of having cancer, in accordance with conventional Northern hybridization techniques known to those persons of ordinary skill in the art. This Northern assay uses a hybridization probe, e.g. radiolabelled TADG-14 cDNA, either containing the full-length, single stranded DNA having a sequence complementary to SEQ ID NO: 6 (Figure 6), or a fragment of that DNA sequence at least 20 (preferably at least 30, more preferably at least 50, and most preferably at least 100 consecutive nucleotides in length). The DNA hybridization probe can be labelled by any of the many different methods known to those skilled in this art.

Antibodies to the TADG-14 protein can be used in an immunoassay to detect increased levels of TADG-14 protein expression in tissues suspected of neoplastic transformation. These same uses can be achieved with Northern blot assays and analyses.

The present invention is directed to DNA encoding a TADG-14 protein selected from the group consisting of: (a) isolated DNA which encodes a TADG-14 protein; (b) isolated DNA which hybridizes to isolated DNA of (a) above and which encodes a TADG-14 protein; and (c) isolated DNA differing from the isolated DNAs of (a) and (b) above in codon sequence due to the degeneracy of the genetic code, and which encodes a TADG-14 protein. Preferably, the DNA has the sequence shown in SEQ ID No. 6. More preferably, the DNA encodes a TADG-14 protein having the amino acid sequence shown in SEQ ID No. 7.

The present invention is also directed to a vector capable of expressing the DNA of the present invention adapted for expression in a recombinant cell and regulatory elements necessary for expression of the DNA in the cell. Preferably, the vector contains DNA encoding a TADG-14 protein having the amino acid sequence shown in SEQ ID No. 7.

The present invention is also directed to a host cell transfected with the vector described herein, said vector expressing a TADG-14 protein. Representative host cells include consisting of bacterial cells, mammalian cells and insect cells.

The present invention is also directed to a isolated and purified TADG-14 protein coded for by DNA selected from the group consisting of: (a) isolated DNA which encodes a TADG-14 protein; (b) isolated DNA which hybridizes to isolated DNA of (a) above and which encodes a TADG-14 protein; and (c) isolated DNA differing from the isolated DNAs of (a) and (b) above in codon sequence due to the degeneracy of the genetic code, and which encodes a TADG-14 protein. Preferably, the isolated and purified TADG-14 protein of claim 9 having the amino acid sequence shown in SEQ ID No. 7.

The present invention is also directed to a method of detecting expression of the protein of claim 1, comprising the steps of: (a) contacting mRNA obtained from the cell with the labeled hybridization probe; and (b) detecting hybridization of the probe with the mRNA.

The following examples are given for the purpose of illustrating various embodiments of the invention and are not meant to limit the present invention in any fashion.

EXAMPLE 1

Tissue collection and storage

Upon patient hysterectomy, bilateral salpingo-oophorectomy, or surgical removal of neoplastic tissue, the specimen is retrieved and placed it on ice. The specimen was then taken to the resident pathologist for isolation and identification of specific tissue samples. Finally, the sample was frozen in liquid nitrogen, logged into the laboratory record and stored at -80°C. Additional specimens were frequently obtained from the Cooperative Human Tissue Network (CHTN). These samples were prepared by the CHTN and shipped to us on dry ice. Upon arrival, these specimens were logged into the laboratory record and stored at -80°C.

EXAMPLE 2

mRNA isolation and cDNA synthesis

Messenger RNA (mRNA) isolation was performed according to the manufacturer's instructions using the Mini RiboSepTM Ultra mRNA isolation kit purchased from Becton Dickinson (cat. # 30034). This was an oligo(dt) chromatography based system of mRNA isolation. The amount of mRNA recovered was quantitated by UV spectrophotometry.

First strand complementary DNA (cDNA) was synthesized using 5.0 mg of mRNA and either random hexamer or oligo(dT) primers according to the manufacturer's protocol utilizing a first strand synthesis kit obtained from Clontech (cat.# K1402-1). The purity of the cDNA was evaluated by PCR using primers

specific for the p53 gene. These primers span an intron such that pure cDNA can be distinguished from cDNA that is contaminated with genomic DNA.

EXAMPLE 3

PCR reactions

Reactions were carried out as follows: first strand cDNA generated from 50 ng of mRNA will be used as template in the presence of 1.0 mM MgCl2, 0.2 mM dNTPs, 0.025 U Taq polymerase/ml of reaction, and 1x buffer supplied with enzyme. In addition, primers must be added to the PCR reaction. Degenerate primers which may amplify a variety of cDNAs are used at a final concentration of 2.0 mM each, whereas primers which amplify specific cDNAs are added to a final concentration of 0.2 mM each.

After initial denaturation at 95°C for 3 minutes, thirty cycles of PCR are carried out in a Perkin Elmer Gene Amp 2400 thermal cycler. Each cycle consists of 30 seconds of denaturation at 95°C, 30 seconds of primer annealing at the appropriate annealing temperature*, and 30 seconds of extension at 72°C. The final cycle will be extended at 72°C for 7 minutes. To ensure that the reaction succeeded, a fraction of the mixture will be electrophoresed through a 2% agarose/TAE gel stained with ethidium bromide(final concentration 1 mg/ml). The annealing temperature varies according to the primers that are used in the PCR reaction. For the reactions involving degenerate primers, an annealing temperature of 48°C were used. The appropriate

annealing temperature for the TADG14 and β-tubulin specific primers is 62°C.

EXAMPLE 4

T-vector ligation and transformations

The purified PCR products are ligated into the Promega T-vector plasmid and the ligation products are used to transform JM109 competent cells according to the manufacturer's instructions (Promega cat. #A3610). Positive colonies were cultured for amplification, the plasmid DNA isolated by means of the WizardTM Minipreps DNA purification system (Promega cat #A7500), and the plasmids were digested with ApaI and SacI restriction enzymes to determine the size of the insert. Plasmids with inserts of the size(s) visualized by the previously described PCR product gel electrophoresis were sequenced.

EXAMPLE 5

DNA sequencing

Utilizing a plasmid specific primer near the cloning site, sequencing reactions were carried out using PRISMTM Ready Reaction Dye DeoxyTM terminators (Applied Biosystems cat# 401384) according to the manufacturer's instructions. Residual dye terminators were removed from the completed sequencing reaction using a Centri-sepTM spin column (Princeton Separation cat.# CS-901). An Applied Biosystems Model 373A DNA Sequencing System was available and was used for sequence analysis. Based upon the determined sequence, primers that

specifically amplify the gene of interest were designed and synthesized.

EXAMPLE 6

Northern blot analysis

mRNAs (approximately 5 mg) were size separated by electrophoresis through a 6.3% formaldehyde, 1.2% agarose gel in 0.02 M MOPS, 0.05 M sodium acetate (pH 7.0), and 0.001 M EDTA. The mRNAs were then blotted to Hybond-N (Amersham) by capillary action in 20x SSPE. The RNAs are fixed to the membrane by baking for 2 hours at 80°C. Additional multiple tissue northern (MTN) blots were purchased from CLONTECH Laboratories, Inc. These blots include the Human MTN blot (cat.#7760-1), the Human MTN II blot (cat.#7759-1), the Human Fetal MTN II blot (cat.#7756-1), and the Human Brain MTN III blot (cat.#7750-1). The appropriate probes were radiolabelled utilizing the Prime-a-Gene Labelling System available from Promega (cat#U1100). The blots were probed and stripped according to the ExpressHyb Hybridization Solution protocol available from CLONTECH (cat.#8015-1 or 8015-2).

EXAMPLE 7

Quantitative PCR

Quantitative-PCR was performed in a reaction mixture consisting of cDNA derived from 50 ng of mRNA, 5 pmol of sense and antisense primers for TADG14 and the internal control β-tubulin, 0.2 mmol of dNTPs, 0.5 mCi of [α-32P]dCTP, and 0.625 U of

Taq polymerase in 1x buffer in a final volume of 25 ml. This mixture was subjected to 1 minute of denaturation at 95°C followed by 30 cycles of denaturation for 30 seconds at 95°C, 30 seconds of annealing at 62°C, and 1 minute of extension at 72°C with an additional 7 minutes of extension on the last cycle. The product was electrophoresed through a 2% agarose gel for separation, the gel was dried under vacuum and autoradiographed. The relative radioactivity of each band was determined by PhosphoImager from Molecular Dynamics.

EXAMPLE 8

The present invention describes the use of primers directed to conserved areas of the serine protease class to identify members of that class which are overexpressed in carcinoma. Several genes were identified and cloned in other tissues, but not previously associated with ovarian carcinoma. The present invention describes a novel protease identified in ovarian carcinoma. This gene was identified using primers to the conserved area surrounding the catalytic domain amino acid histidine and the catalytic domain amino acid serine which is about 150 amino acids downstream towards the carboxyl end.

The gene encoding the novel extracellular serine protease of the present invention was identified from a group of proteases overexpressed in carcinoma by subcloning and sequencing the appropriate PCR products. An example of such a PCR reaction is given in Figure 1. Subcloning and sequencing of individual bands from such an amplification provided a basis for identifying the novel protease of the present invention.

EXAMPLE 9

The sequence determined for the catalytic domain of TADG-14 is presented in Figure 2 and is consistent with other serine proteases and specifically contains conserved amino acids appropriate for the catalytic domain of the serine protease family. Specific primers (20mers) derived from this sequence were used.

A series of normal and tumors cDNAs were examined to determine the expression of the TADG-14 protein. In a series of three normals compared to nine carcinomas using β-tubulin as an internal control for PCR amplification, TADG-14 was significantly overexpressed in eight of the nine carcinomas and either was not detected or was detected at a very low level in normal epithelial tissue (Figure 3). This evaluation was extended to a standard panel of about 35 tumors. Using these specific primers, the expression of this gene was also examined in both tumor cell lines and other tumor tissues as shown in Figure 4. The expression of TADG-14 was also observed in breast carcinoma and colon carcinoma. TADG-14 expression was not noted in other tissues. For example, TADG-14 was not present in detectable levels by Northern blot analysis in any of the following normal tissues: fetal lung, fetal heart, fetal brain, fetal kidney, adult spleen, thymus, prostate, testis, ovary, small intestine, colon, peripheral blood leukocytes, heart, placenta, lung, liver, skeletal muscle, kidney, pancreas, amygdala, caudate nucleus, corpus callosum, hippocampus, whole brain, subthalamic nucleus and thalamus.

Using the specific sequence for TADG-14 covering the full domain of the catalytic site as a probe for Northern blot analysis, three Northern blots were examined: one derived from

ovarian tissues, both normal and carcinoma; one from fetal tissues; and one from adult normal tissues. As noted in Figure 5, abundant transcripts for TADG-14 were noted in ovarian carcinomas. Transcripts were noted in all carcinomas, but at lower levels in some sub-types of ovarian cancer. Furthermore, no transcript was observed from normal ovarian tissue. The transcript size was found to be approximately 1.4 kb. Of particular note is the fact that in the fetal tissue examined including brain, lung, liver, kidney and in multiple adult tissues examined, none of these blots showed expression for the TADG-14 transcript. The hybridization for the fetal and adult blots was appropriate and done with the same probe as with the ovarian tissue. Subsequent to this examination, it was confirmed that these blots contained other detectible mRNA transcripts

Using the base sequence derived from the original full length PCR clone corresponding to nucleotides 713-1160 of the catalytic domain as a probe to screen libraries, an ovarian carcinoma library derived from ascites tumor cells was examined for the presence of TADG-14. Four clones were obtained, two of which covered the complete mRNA 1.4kb transcript of the TADG-14 gene. The complete nucleotide sequence (SEQ ID No:6) is provided in Figure 6 along with translation of the open reading frame (SEQ ID No:7).

In the nucleotide sequence, there is a Kozak sequence typical of sequences upstream from the initiation site of translation. There is also a polyadenylation signal sequence and a poly-A tail. The open reading frame consists of a 260 amino acid sequence (SEQ ID No:7) which includes a secretion signal sequence in the first 25 amino acids confirming the extracellular processing

of the protease. Also a clear delineation of the catalytic domain conserved histidine, aspartic acid, serine series along with a series of amino acids conserved in the serine protease family is indicated.

Examination of the databases for both the expressed tag sequence and complete transcripts provided seven genes that had significant homology to this newly identified serine protease. One gene was identified from mouse brain and a comparison of the nucleotide homology is provided in Figure 7. A comparison of the homology of the amino acid sequence is provided in Figure 8. Alignment of TADG-14 with mouse neuropsin revealed 77.2% similarity and 72.2% identity at the amino acid levels for these two genes. Given that the size of the mouse transcript is 1.4kb and that the mouse gene contains 260 amino acids and there is greater than 70% homology, this gene may be a human equivalent of the mouse neuropsin gene or a member of neuropsin-like genes.

TADG-14 is secreted and expressed early in tumor development and has invasive capacity. TADG-14 therefore is a potential diagnostic for ovarian and other cancers. TADG-14 also may be a target for intervention in regulating tumor spread by inhibition, gene therapy, antibody inactivation technology. In addition to its obvious usefulness in ovarian carcinoma and other carcinomas including the preliminary data on breast and prostate, the neuropsin-like qualities may provide an opportunity for usefulness in neuropathologic disorders.

EXAMPLE 10

To identify the expressed serine proteases, degenerate oligodeoxynucleotide primers designed to the conserved amino

acid sequences surrounding the invariant His and Ser residues of the catalytic triad were used in PCR reactions with cDNA from either normal ovarian tissue or ovarian carcinoma as the template. PCR products of the appropriate size were subcloned into T-vector and sequenced. Among proteases already identified using this strategic approach e.g. hepsin and stratum corneum chymotryptic enzyme (SCCE) have been shown to be expressed at abnormally high levels in ovarian carcinoma. Homology searches for this novel protease TADG14 revealed that one of the subclones obtained from ovarian carcinoma represented a novel 406 base pair (bp) sequence that has significant sequence similarity to other known proteases including mouse neuropsin, human glandular kallikrein and human PSA. The complete cDNA for this novel sequence was cloned and found to encode a trypsin like serine protease, named TADG14. More importantly, the TADG14 transcript was found to be highly expressed in a majority of ovarian tumors but not expressed by normal ovarian tissue. High level expression of TADG14 appears to be restricted to tumors, and this protease appears to be secreted in a manner that would suggest a possible role in invasion and metastasis. Moreover, due to the extracellular nature of this enzyme, it may be possible to exploit its expression as a diagnostic tool for ovarian cancer.

Using the novel 406 bp sequence as a probe, Northern blot analysis was carried out to determine the transcript size and tissue specificity of its expression. It was found that the mRNA for this clone is approximately 1.4 kilobases (kb) (Fig. 9A), and that it is strongly expressed in ovarian carcinomas but not in normal ovary. More importantly, the transcript was found to be undetectable by Northern analysis in 28 normal human tissues

studied (Fig. 9B, 9C, 9D some data not shown). In a more sensitive assay of 50 normal human tissues (Clontech) RNA dot blot analysis revealed that this clone was very weakly expressed in only three of these 50 tissues, kidney, lung and mammary gland (data not shown).

Using standard hybridization techniques, a cDNA library constructed from the mRNA isolated from the ascites cells of an ovarian cystadenocarcinoma patient was screened. Five clones were obtained, two of which overlapped and spanned 1343 nucleotides (Fig. 10A). The last two nucleotides prior to the poly (A) tail and the poly (A) tail itself were obtained from the EST database available at NCBI (accession #AA343629). Subsequent Northern blot analyses with probes derived from sequences near the 5' or 3' end of this cDNA were consistent with previous results suggesting that the obtained clones were produced by the same gene (data not shown). This cDNA includes a Kozak's consensus sequence for the initiation of translation, and a polyadenylation signal. The mRNA provides an open reading frame of 260 amino acids, which contains the necessary residues (His^{73}, Asp^{120}, Ser^{212}) in the appropriate context to classify this protein as a trypsin-like serine protease. Near its amino-terminus, the predicted protein contains a stretch of hydrophobic amino acids that may act as a secretion signal sequence. In addition, residues 110 to 112 encode a potential site for glycosylation that is common to serine proteases of the kallikrein subfamily such as PSA. This enzyme was named TADG14. Comparison of the deduced TADG14 amino acid sequence with sequences of known proteases revealed that it possesses significant similarity with human glandular kallikrein (hHk2), PSA, Protease M and mouse neuropsin. At the

amino acid level TADG14 is 48% identical to Protease M, 46% identical to hHk2, and 43% identical to PSA. More interestingly, the mouse protease neuropsin and TADG14 share 72% amino acid identity. In addition to the similarity of the protein sequences, neuropsin and TADG14 mRNAs are of similar size (1.4 kb) and structure with approximately the same amounts of 5' and 3' untranslated regions suggesting the possibility of orthology. Neuropsin was originally cloned from mouse hippocampus and shown to be differentially expressed under stimulation. However, TADG14 mRNA was undetectable in human hippocampus by Northern blot (data not shown).

To characterize the extent and frequency of expression of the TADG14 gene in ovarian tumors quantitative PCR was utilized with cDNA derived from normal ovary, ovarian carcinoma or low malignant potential (LMP) tumors as template. This technique has been previously authenticated and verified by Northern blot and Western blot. PCR primers that amplify a TADG14 specific 230 bp product were synthesized and used simultaneously in reactions with primers that produce a specific 454 bp PCR product for ß-tubulin. For TADG14 specific PCR the primers were: sense, 5'-ACAGTACGCCTGGG AGACCA-3'; antisense, 5'-CTGAGACGGTGCAATTCTGG-3'. The tubulin primers were as described in ref. 11. Reactions were carried out as follows: first strand cDNA generated from 50ng of mRNA was used as template in the presence of 1.0mM $MgCl_2$, 0.2mM dNTPs, 0.025 U *Taq* polymerase/ml of reaction, and 1x buffer supplied with enzyme. Primers which amplify specific cDNAs are added to a final concentration of 0.2mM each. After initial denaturation at 95 C for 3 minutes, thirty cycles of PCR were carried out in a Perkin Elmer

Gene Amp 2400 thermal cycler. Each cycle consists of 30 seconds of denaturation at 95 C, 30 seconds of primer annealing at 62 C and 30 seconds of extension at 72 C. The final cycle was extended at 72 C for 7 minutes. A radiolabelled nucleotide was included in this reaction, the PCR products were separated on a 2% agarose gel and the intensity of each band was quantitated by a Phosphoimager (Molecular Dynamics). Figure 11A shows an ethidium bromide stained agarose gel with the separated quantitative PCR products and is representative of the typical results observed.

The ratio of the TADG14 PCR product to that of ß-tubulin (mean ± SD) was calculated for normal ovary (0.034 ± 0.024) samples which all showed relatively low expression levels. TADG14 overexpression was defined as exceeding the mean of the ratio of TADG14 to ß-tubulin for normal samples by greater than 2 standard deviations (SD). TADG14 was found to be overexpressed in 4 of 10 LMP tumors (40%), and 20 of 30 ovarian carcinomas (67%) studied. For individual histologic subtypes of tumor, the expression ratio was 0.110 ± 0.092 for serous LMP tumors, 0.096 ± 0.142 for mucinous LMP tumors, 0.457 ± 0.345 for serous carcinomas, 0.171± 0.300 for mucinous carcinomas, 0.308 ± 0.144 for clear cell carcinomas, and 0.485 ± 0.325 for endometrioid carcinomas. Of the 30 carcinomas studied, 13 of 17 serous tumors, 1 of 7 mucinous tumors, 3 of 3 clear cell tumors and 3 of 3 endometrioid tumors overexpressed TADG14 (Fig. 11B).

Immunogenic poly-lysine linked multiple antigen peptides were synthesized based on the deduced amino acid sequence of TADG14 and used to immunize rabbits for the production of polyclonal antibodies. The antiserum raised to the

peptide sequence LDWIKKIIGSKG was used in western blot analysis to determine if this antibody would recognize a protein of the predicted size of 28kDa. Proteins from the cervical cancer derived HeLa cell line and the breast carcinoma derived MD-MBA-435S cell line were used in this experiment and it was found that the antibody recognized a single 30 kDa protein in both (Fig. 12A, lanes 3 and 4). This size is within a reasonable range of the predicted molecular weight. As a negative control, duplicate HeLa and MD-MB435S lysates were examined with rabbit pre-immune serum (Fig. 12A, lanes 1 and 2). More importantly, this experiment was reproducible with antisera to a peptide from a different region of TADG14, suggesting that cultured cancer cells produce the TADG14 protein.

Immunohistochemical staining supported the data obtained by quantitative PCR and by Northern blot as shown in Figure 13. Using a TADG14 peptide directed antibody, no staining was observed with normal ovarian tissue samples. However, intense staining was associated with tumor cells of all of the various histological subtypes of ovarian carcinoma examined. For serous carcinoma, the antigen appears to be associated with tumor cells in the form of granules. These granular structures may be intermediates in the pathway that ultimately leads to secretion of TADG14. In mucinous and clear cell carcinoma samples, TADG14 is highly associated with the tumor cells. In endometrioid carcinoma, the antigen is most prevalent in the glandular lumen formed by the tumor cells.

The lethality of cancer cells lies in their ability to proliferate abnormally and invade normal host tissues. Malignancies employ proteases to provide a variety of services

that assist in the process of tumor progression including activation of growth and angiogenic factors and to provide the basis for invasion and metastasis. In the process of studying these enzymes, overexpression of the known proteases, hepsin and SCCE was identified. In the present study, a cDNA was cloned encoding a novel serine protease, TADG14. This protease was found to be very highly expressed in 67% (20/30) of ovarian carcinomas studied, whereas it was undetected in normal ovarian tissue. No detection the TADG14 transcript at levels similar to tumor samples in any of 50 normal human tissues studied was seen. This suggests the possibility that this gene is under the control of a promoter that is most active in ovarian tumors, and it may be possible to exploit this for therapeutic means.

At the amino acid level, TADG14 most closely resembles a mouse protease known as neuropsin, which was originally cloned from mouse hippocampus. Neuropsin has been implicated in neuronal plasticity, which suggests that TADG14 may very well be capable of restructuring the three-dimensional architecture of a tumor allowing for shedding of tumor cells or invasion of normal host tissues. Immunohistochemical staining of ovarian tumors revealed that TADG14 is highly associated with tumor cells and the cells near the invasive fronts of tumor cells. Therefore, TADG14 is an important target for the inhibition of tumor progression.

Most importantly, the five-year survival rate for ovarian cancer patients remains below 50% because of an inability to diagnose this disease at an early stage. TADG14 contains a secretion signal sequence and immunohistochemical data suggest that TADG14 is secreted. In addition, by Northern blot and RNA

dot blot analyses, TADG14 appears to be rather tumor specific. As a result of this, it may be possible to design assays based on the detection of this protein for the early detection of ovarian cancer. Currently, the best available ovarian cancer tumor marker is CA125. However, due to high endogenous circulating levels of this antigen, the signal to noise ratio limits its usefulness as a diagnostic tool. Therefore, TADG14, due to its limited expression in other tissues, may prove to be a valuable tool for diagnosing ovarian cancer, especially the most prevalent serous cystadenocarcinoma subtype.

Any patents or publications mentioned in this specification are indicative of the levels of those skilled in the art to which the invention pertains. These patents and publications are herein incorporated by reference to the same extent as if each individual publication was specifically and individually indicated to be incorporated by reference.

One skilled in the art will readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The present examples along with the methods, procedures, treatments, molecules, and specific compounds described herein are presently representative of preferred embodiments, are exemplary, and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention as defined by the scope of the claims.

WHAT IS CLAIMED IS:

1. DNA encoding a TADG-14 protein selected from the group consisting of:

(a) isolated DNA which encodes a TADG-14 protein;

(b) isolated DNA which hybridizes to isolated DNA of (a) above and which encodes a TADG-14 protein; and

(c) isolated DNA differing from the isolated DNAs of (a) and (b) above in codon sequence due to the degeneracy of the genetic code, and which encodes a TADG-14 protein.

2. The DNA of claim 1, wherein said DNA has the sequence shown in SEQ ID No. 6.

3. The DNA of claim 1, wherein said TADG-14 protein has the amino acid sequence shown in SEQ ID No. 7.

4. A vector capable of expressing the DNA of claim 1 adapted for expression in a recombinant cell and regulatory elements necessary for expression of the DNA in the cell.

5. The vector of claim 4, wherein said DNA encodes a TADG-14 protein having the amino acid sequence shown in SEQ ID No. 7.

6. A host cell transfected with the vector of claim 4, said vector expressing a TADG-14 protein.

7. The host cell of claim 6, wherein said cell is selected from group consisting of bacterial cells, mammalian cells, plant cells and insect cells.

8. The host cell of claim 7, wherein said bacterial cell is *E. coli*.

9. Isolated and purified TADG-14 protein coded for by DNA selected from the group consisting of:

(a) isolated DNA which encodes a TADG-14 protein;

(b) isolated DNA which hybridizes to isolated DNA of (a) above and which encodes a TADG-14 protein; and

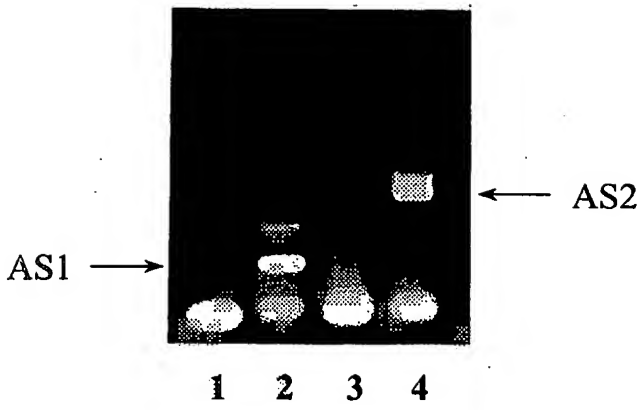
(c) isolated DNA differing from the isolated DNAs of (a) and (b) above in codon sequence due to the degeneracy of the genetic code, and which encodes a TADG-14 protein.

10. The isolated and purified TADG-14 protein of claim 9 having the amino acid sequence shown in SEQ ID No. 7.

11. A method of detecting expression of the protein of claim 1, comprising the steps of:

(a) contacting mRNA obtained from the cell with the labeled hybridization probe; and

(b) detecting hybridization of the probe with the mRNA.



1) Normal Ovary 2) Tumor
3) Normal Ovary 4) Tumor

FIGURE 1

```
201        PRIMER                                                              250
  Prom    WVLTAAHC KK   PNLQV....F   LGKHNLRQRE   SSQEQSSVVR   AVIHPDY...
Tadg14    WVVTAAHC KK   PKYTV....R   LGDHSLQNKD   GPEQEIPVVQ   SIPHPCY...
  Try1    WVVSAGHC YK   SRIQV....R   LGEHNIEVLE   GNEQFINAAK   IIRHPQY...
  Scce    WVLTAAHC KM   NEYTV....H   LGSDTLGDRR   A..QRIKASK   SFRHPGY...
  Heps    WVLTAAHC FP   ERNRVLSRWR   VFAGAVAQAS   PHGLGLGVQA   VVYHGGYLFF

          251                                                             300
  Prom    ...DAASHDQ   DIMLL RLARP   AKLSELIQPL   PLERDCSA..   NTTSCHILGW
Tadg14    NSSDVEDHNH   DLMLL QLRDQ   ASLGSKVKPI   SLADHCTQ..   PGQNCTVSGW
  Try1    ...DRKTLNN   DIMLI KLSSR   AVINARVSTI   SLPTAPPA..   TGTKCLISGW
  Scce    ST...QTHVN   DLMLV KLNSQ   ARLSSMVKKV   RLPSRCEP..   PGTTCTVSGW
  Heps    RDPNSEENSN   DIALV HLSSP   LPLTEYIQPV   CLPAAGQALV   DGKICTVTGW

          301                                                         350
  Prom    GKTAD..GDF   PDTIQCAYIH   LVSREECEHA   ..TPGQITQN   MLCAGDEKYG
Tadg14    GTVTSPRENF   PDTLNCAEVK   IFPQKKCEDA   ..YPGQITDG   MVCAGSSK.G
  Try1    GNTASSGADY   PDELQCLDAP   VLSQAKCEAS   ..YPGKITSN   MFCVGFLEGG
  Scce    GTTTSPDVTF   PSDLMCVDVK   LISPQDCTKV   ..YKDLLENS   MLCAGIPDSK
  Heps    GNTQYYGQQ.   AGVLQEARVP   IISNDVCNGA   DFYGNQIKPK   MFCAGYPEGG

          351
  Prom    KDSCQ GDSGG     SEQ ID No. 1
Tadg14    ADTCQ GDSGG     SEQ ID No. 2
  Try1    KDSCQ GDSGG     SEQ ID No. 3
  Scce    KNACN GDSGG     SEQ ID No. 4
  Heps    IDACQ GDSGG     SEQ ID No. 5
                PRIMER
```

FIGURE 2

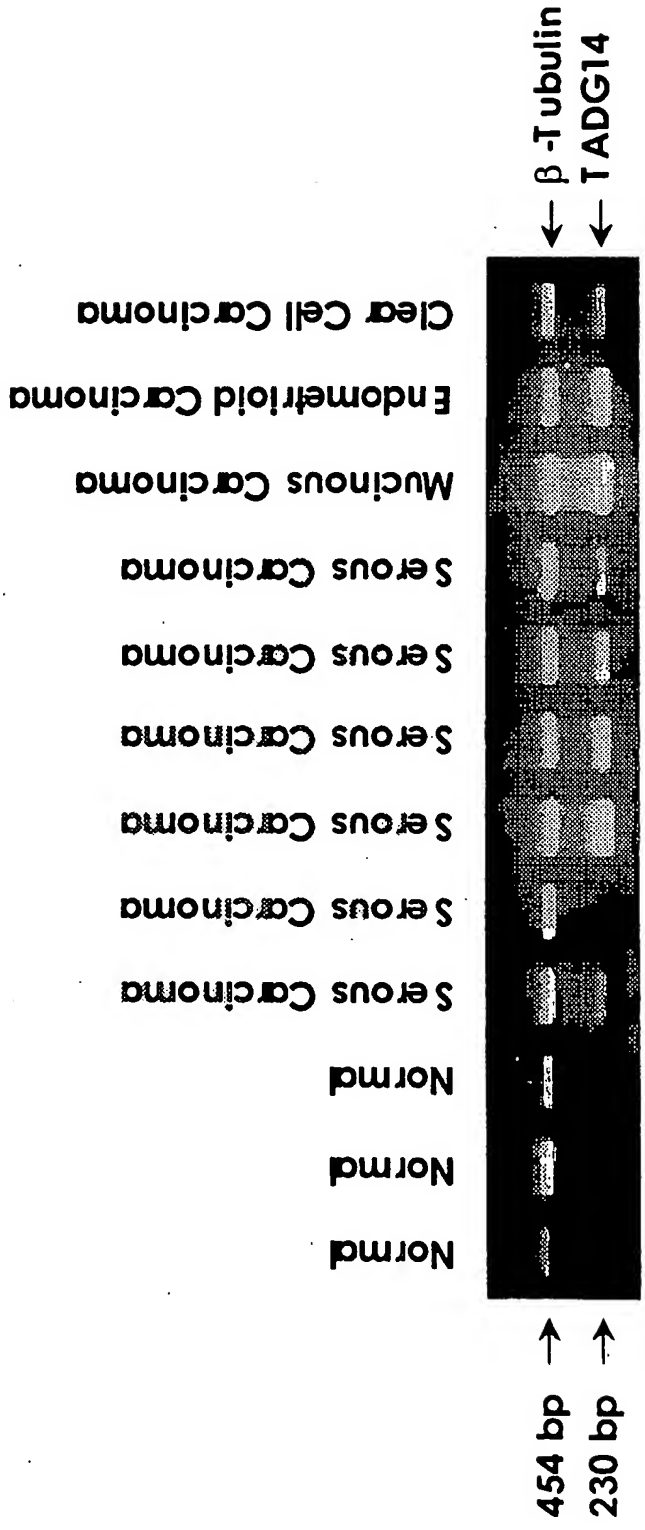

β-Tubulin
TADG14
Clear Cell Carcinoma
Endometrioid Carcinoma
Mucinous Carcinoma
Serous Carcinoma
Serous Carcinoma
Serous Carcinoma
Serous Carcinoma
Serous Carcinoma
Normal
Normal
Normal
454 bp
230 bp

FIGURE 3

β - Tubulin
TADG 14
Ovarian Carcinoma CL Caov - 3
Ovarian Carcinoma CL SWS 626
Breast Carcinoma CL MDA-MB-435S
Breast Carcinoma CL MDA-MB-231
Breast Carcinoma
Prostate Carcinoma
Colon Carcinoma
Normal Colon
454 bp
230 bp

FIGURE 4

TADG14
1.4kb
Normal Ovary
Serous Carcinoma
Mucinous Carcinoma
Endometrioid Carcinoma
Clear Cell Carcinoma
Brain
FETAL
Lung
Liver
Kidney
Spleen
Thymus
Prostate
Testes
Ovary
Small Intestine
Colon
P.B. Leukocyte *
ADULT
* P.B. : Peripheral Blood

FIGURE 5

```
   1  CTGTAGCAGGCAGAGCTTACCAAGTCTCTCCGAACTCAAATGGAAGAAATACCTTATGAA   60
  61  TGTAAGAATGTAGGGGGTCATGGCTTGTAATTTACACAGTGTAAATGAAACCATCCTAGA  120
 121  GGATTATGAGGAATCCTTTCTATGTGATTTTCAATCATAGCAAGCAAGAAAGGCTCCAGT  180
 181  GTCAAGGTAGTTCAGCTCTTACAGGATATAAAACAGTCCATACTTGAGAGAAAAAACTTA  240
 241  GATCTGAGTGATGGAATGTGAAGCAAATCTTTCAAAATCAGTAGACATTTCTTGGACATA  300
 301  AAACACAGATGAGGAAAGGGCTTCAAATTAGAAGTTACGTAATCACCATCAGAAAGTTCA  360
 361  TGTTTGGTAAATTCTGTTACTAGAAATGTAGGAAATTCAGGTATAGCTTTGAATCCCAAT  420
 421  TACACATTGGTCAGTGGGAAAACTAAGGGCCTCCAACAGGCAAATTCAGGGAGGATAGGT  480
 481  TTCAGGGAATGCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGACCTCGTGCGG  540
                                    M  G  R  P  R  P  R  A  A  -
 541  CCAAGACGTGGATGTTCCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGCAC  600
        K  T  W  M  F  L  L  L  L  G  G  A  W  A  G  H  S  R  A  Q  -
 601  AGGAGGACAAGGTGCTGGGGGGTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG  660
        E  D  K  V  L  G  G  H  E  C  Q  P  H  S  Q  P  W  Q  A  A  -
 661  CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCC  720
        L  F  Q  G  Q  Q  L  L  C  G  G  V  L  V  G  G  N  W  V  L  -
 721  TTACAGCTGCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTAC  780
        T  A  A  H+C  K  K  P  K  Y  T  V  R  L  G  D  H  S  L  Q  -
 781  AGAATAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCT  840
        N  K  D  G  P  E  Q  E  I  P  V  V  Q  S  I  P  H  P  C  Y  -
 841  ACAACAGCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACC  900
        N  S  S  D  V  E  D  H  N  H  D+L  M  L  L  Q  L  R  D  Q  -
 901  AGGCATCCCTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTG  960
        A  S  L  G  S  K  V  K  P  I  S  L  A  D  H  C  T  Q  P  G  -
 961  GCCAGAAGTGCACCGTCTCAGGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTTCCTG 1020
        Q  K  C  T  V  S  G  W  G  T  V  T  S  P  R  E  N  F  P  D  -
1021  ACACTCTCAACTGTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACC 1080
        T  L  N  C  A  E  V  K  I  F  P  Q  K  K  C  E  D  A  Y  P  -
1081  CGGGGCAGATCACAGATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCC 1140
        G  Q  I  T  D  G  M  V  C  A  G  S  S  K  G  A  (D)  T  C  Q  -
1141  AGGGCGATTCTGGAGGCCCCCTGGTGTGTGATGGTGCACTCCAGGGCATCACATCCTGGG 1200
        G  D  (S+)  G  G  P  L  V  C  D  G  A  L  Q  G  I  T  S  W  (G)  -
1201  GCTCAGACCCCTGTGGGAGGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACC 1260
        S  D  P  C  G  R  S  D  K  P  (G)  V  Y  T  N  I  C  R  Y  L  -
1261  TGGACTGGATCAAGAAGATCATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCT 1320
        D  W  I  K  K  I  I  G  S  K  G  *  SEQ ID No. 6
1321  CCCTTAATAAACTCACGGAATTC SEQ ID No. 7
```

└──┘ = Kozak's Consensus sequence

\+ = Conserved amino acids of catalytic triad H, D, S

NSS = Possible N - linked glycosylation site

⌒ = Poly - adenylation signal

▭ = Conserved nt of catalytic triad

◯ = aa required for formation of an oxyanion hole for catalytic activity

FLLL = Secretion signal sequence

FIGURE 6

6/17

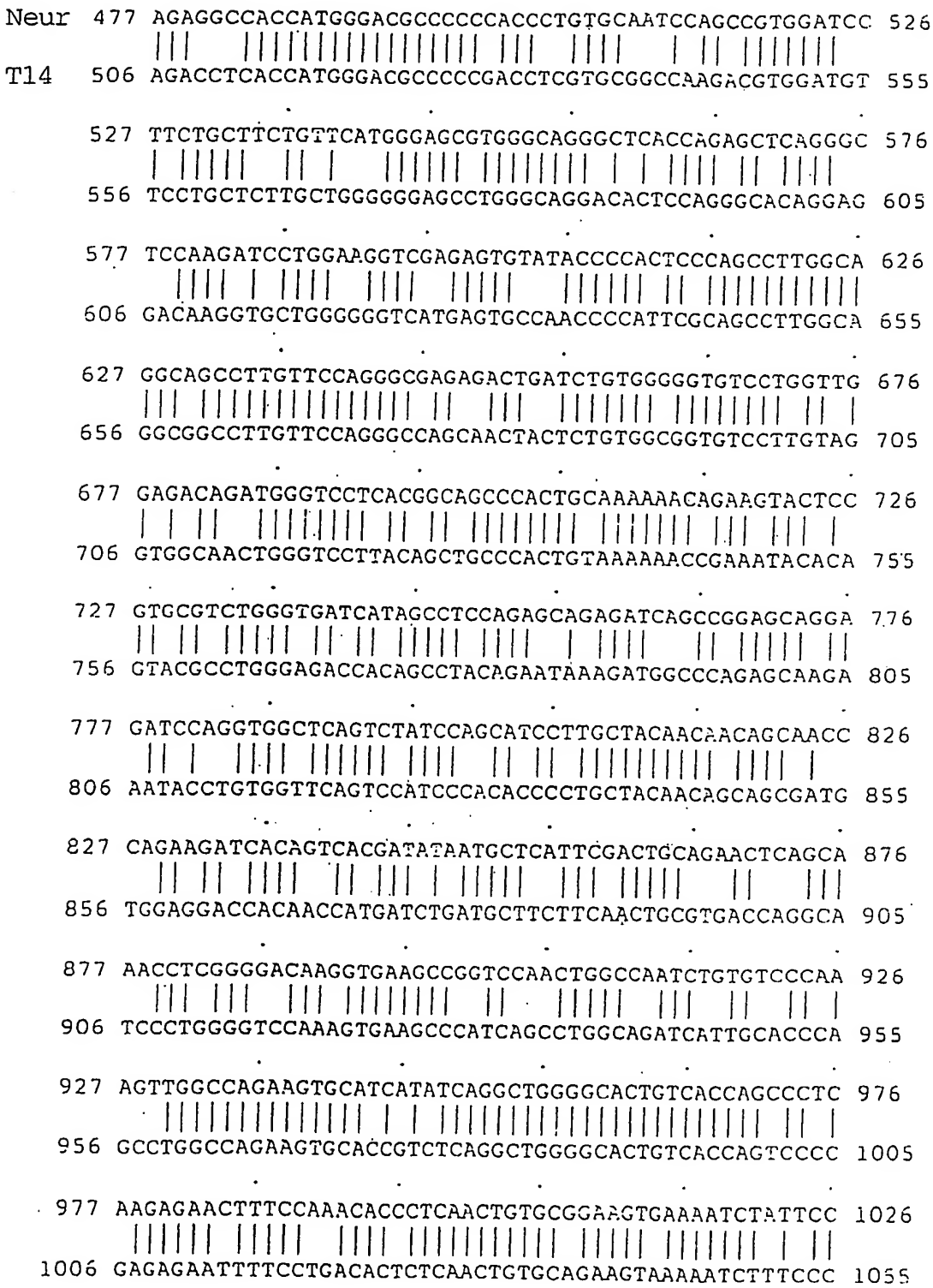
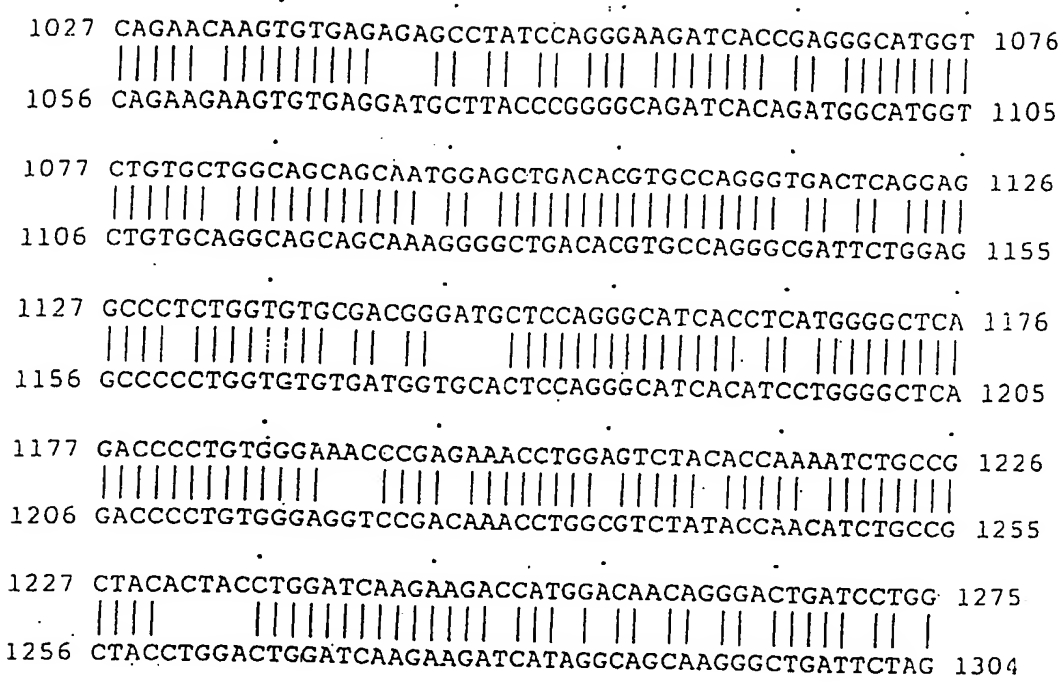

Neur 477 AGAGGCCACCATGGGACGCCCCCCACCCTGTGCAATCCAGCCGTGGATCC 526
T14 506 AGACCTCACCATGGGACGCCCCCGACCTCGTGCGGCCAAGACGTGGATGT 555
527 TTCTGCTTCTGTTCATGGGAGCGTGGGCAGGGCTCACCAGAGCTCAGGGC 576
556 TCCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGCACAGGAG 605
577 TCCAAGATCCTGGAAGGTCGAGAGTGTATACCCCACTCCCAGCCTTGGCA 626
606 GACAAGGTGCTGGGGGGTCATGAGTGCCAACCCCATTCGCAGCCTTGGCA 655
627 GGCAGCCTTGTTCCAGGGCGAGAGACTGATCTGTGGGGGTGTCCTGGTTG 676
656 GGCGGCCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAG 705
677 GAGACAGATGGGTCCTCACGGCAGCCCACTGCAAAAAACAGAAGTACTCC 726
706 GTGGCAACTGGGTCCTTACAGCTGCCCACTGTAAAAAACCGAAATACACA 755
727 GTGCGTCTGGGTGATCATAGCCTCCAGAGCAGAGATCAGCCGGAGCAGGA 776
756 GTACGCCTGGGAGACCACAGCCTACAGAATAAAGATGGCCCAGAGCAAGA 805
777 GATCCAGGTGGCTCAGTCTATCCAGCATCCTTGCTACAACAACAGCAACC 826
806 AATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACAGCAGCGATG 855
827 CAGAAGATCACAGTCACGATATAATGCTCATTCGACTGCAGAACTCAGCA 876
856 TGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCA 905
877 AACCTCGGGGACAAGGTGAAGCCGGTCCAACTGGCCAATCTGTGTCCCAA 926
906 TCCCTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCA 955
927 AGTTGGCCAGAAGTGCATCATATCAGGCTGGGGCACTGTCACCAGCCCTC 976
956 GCCTGGCCAGAAGTGCACCGTCTCAGGCTGGGGCACTGTCACCAGTCCCC 1005
977 AAGAGAACTTTCCAAACACCCTCAACTGTGCGGAAGTGAAAATCTATTCC 1026
1006 GAGAGAATTTTCCTGACACTCTCAACTGTGCAGAAGTAAAAATCTTTCCC 1055

FIGURE 7-1



Neur SEQ ID No. 9

T14 SEQ ID No. 10

FIGURE 7-2

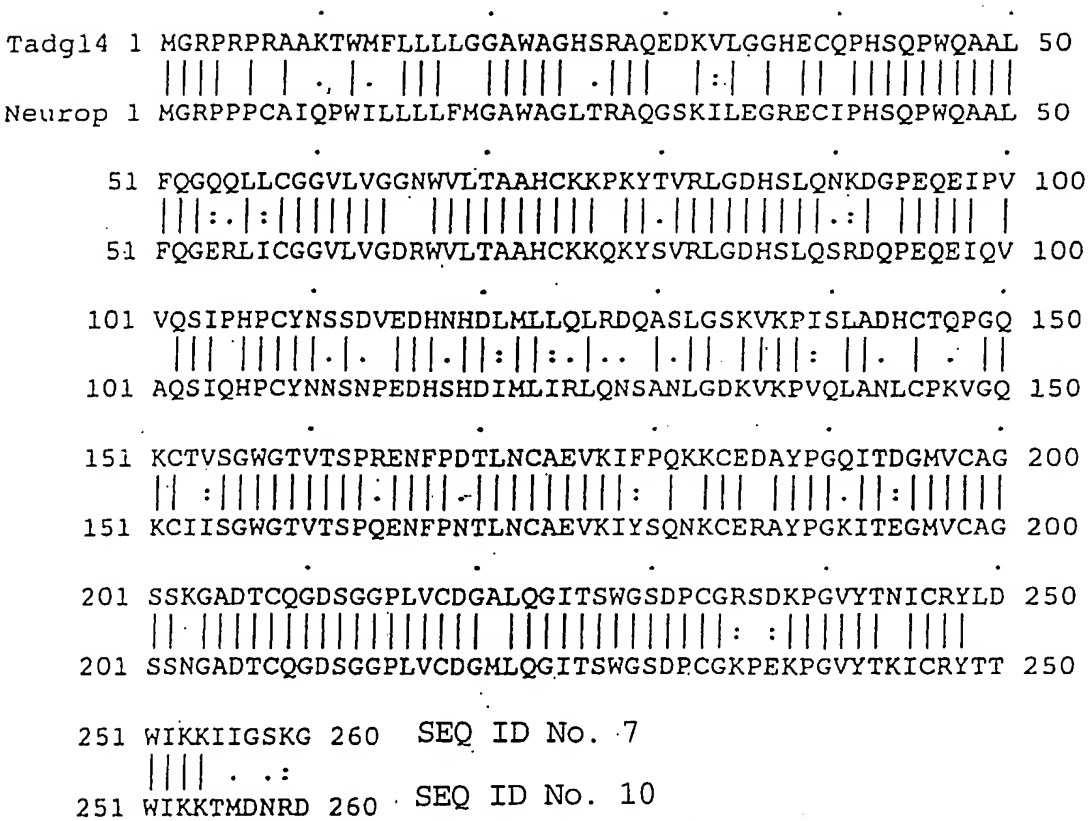

Tadg14 1 MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAAL 50
Neurop 1 MGRPPPCAIQPWILLLLFMGAWAGLTRAQGSKILEGRECIPHSQPWQAAL 50
51 FQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPV 100
51 FQGERLICGGVLVGDRWVLTAAHCKKQKYSVRLGDHSLQSRDQPEQEIQV 100
101 VQSIPHPCYNSSDVEDHNHDLMLLQLRDQASLGSKVKPISLADHCTQPGQ 150
101 AQSIQHPCYNNSNPEDHSHDIMLIRLQNSANLGDKVKPVQLANLCPKVGQ 150
151 KCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQITDGMVCAG 200
151 KCIISGWGTVTSPQENFPNTLNCAEVKIYSQNKCERAYPGKITEGMVCAG 200
201 SSKGADTCQGDSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLD 250
201 SSNGADTCQGDSGGPLVCDGMLQGITSWGSDPCGKPEKPGVYTKICRYTT 250
251 WIKKIIGSKG 260 SEQ ID No. 7
251 WIKKTMDNRD 260 SEQ ID No. 10

FIGURE 8

FETAL
Brain
Lung
Liver
Kidney
Normal Ovary
Serous Carcinoma
Mucinous Carcinoma
Endometrioid Carcinoma
Clear Cell Carcinoma
1.4kb
TADG14
β-tubulin
A
B

FIGURE 9-1

ADULT
Heart
Brain
Placenta
Lung
Liver
Skeletal Muscle
Kidney
Pancreas
Spleen
Thymus
Prostate
Testes
Ovary
Small Intestine
Colon
P.B. Leukocyte *
1.4kb
TADG14
β-tubulin
C
D
* P.B. : Peripheral Blood

FIGURE 9-2

```
   1 CTGTAGCAGGCAGAGCTTACCAAGTCTCTCCGAACTCAAATGGAAGAAATACCTTATGAA
  61 TGTAAGAATGTAGGGGGTCATGGCTTGTAATTTACACAGTGTAAATGAAACCATCCTAGA
 121 GGATTATGAGGAATCCTTTCTATGTGATTTTCAATCATAGCAAGCAAGAAAGGCTCCAGT
 181 GTCAAGGTAGTTCAGCTCTTACAGGATATAAAACAGTCCATACTTGAGAGAAAAAACTTA
 241 GATCTGAGTGATGGAATGTGAAGCAAATCTTTCAAAATCAGTAGACATTTCTTGGACATA
 301 AAACACAGATGAGGAAAGGCTTCAAATTAGAAGTTACGTAATCACCATCAGAAAGTTCA
 361 TGTTTGGTAAATTCTGTTACTAGAAATGTAGGAAATTCAGGTATAGCTTTGAATCCCAAT
 421 TACACATTGGTCAGTGGGAAAACTAAGGGCCTCCAACAGGCAAATTCAGGGAGGATAGGT
 481 TTCAGGGAATGCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGACCTCGTGCGG
                                     M  G  R  P  R  P  R  A  A
 541 CCAAGACGTGGATGTTCCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGCAC
       K  T  W  M  F  L  L  S  L  L  G  G  A  W  A  G  H  S  R  A  Q
 601 AGGAGGACAAGGTGCTGGGGGGTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG
       E  D  K  V  L  G  G  H  E  C  Q  P  H  S  Q  P  W  Q  A  A
 661 CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCC
       L  F  Q  G  Q  Q  L  L  C  G  G  V  L  V  G  G  N  W  V  L
 721 TTACAGCTGCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTAC
       T  A  A  H  C  K  K  P  K  Y  T  V  R  L  G  D  H  S  L  Q
 781 AGAATAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCT
       N  K  D  G  P  E  Q  E  I  P  V  V  Q  S  I  P  H  P  C  Y
 841 ACAACAGCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACC
       N  S  S  D  V  E  D  H  N  H  D  L  M  L  L  Q  L  R  D  Q
 901 AGGCATCCCTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTG
       A  S  L  G  S  K  V  K  P  I  S  L  A  D  H  C  T  Q  P  G
 961 GCCAGAAGTGCACCGTCTCAGGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTTCCTG
       Q  K  C  T  V  S  G  W  G  T  V  T  S  P  R  E  N  F  P  D
1021 ACACTCTCAACTGTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACC
       T  L  N  C  A  E  V  K  I  F  P  Q  K  K  C  E  D  A  Y  P
1081 CGGGGCAGATCACAGATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCC
       G  Q  I  T  D  G  M  V  C  A  G  S  S  K  G  A  D  T  C  Q
1141 AGGGCGATTCTGGAGGCCCCCTGGTGTGTGATGGTGCACTCCAGGGCATCACATCCTGGG
       G  D  S  G  G  P  L  V  C  D  G  A  L  Q  G  I  T  S  W  G
1201 GCTCAGACCCCTGTGGGAGGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACC
       S  D  P  C  G  R  S  D  K  P  G  V  Y  T  N  I  C  R  Y  L
1261 TGGACTGGATCAAGAAGATCATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCT
       D  W  I  K  K  I  I  G  S  K  G  *  SEQ ID No. 7
1321 CCCTTAATAAACTCACAACTCTC  SEQ ID No. 6
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FIGURE 10-1

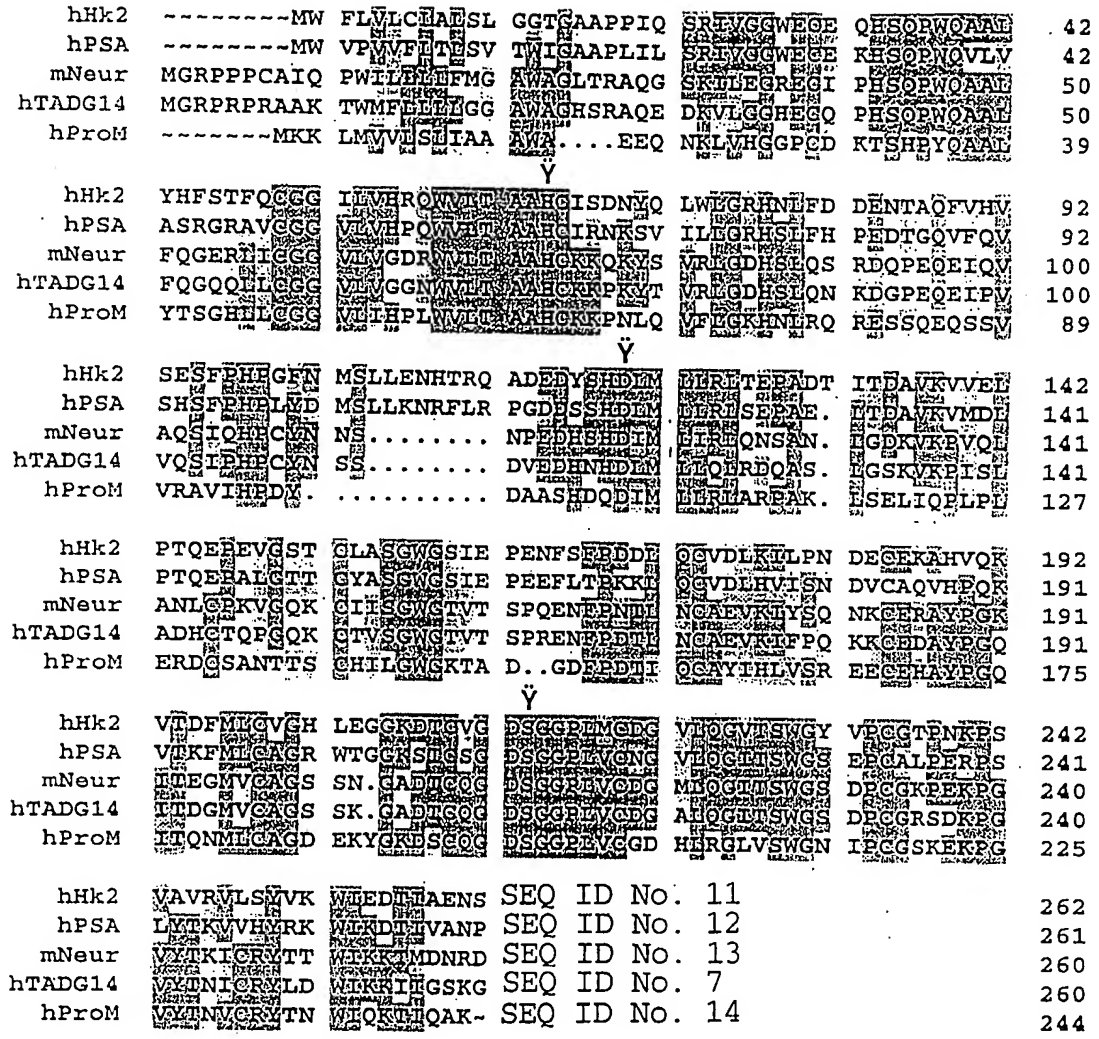
hHk2
hPSA
mNeur
hTADG14
hProM
SEQ ID No. 11
SEQ ID No. 12
SEQ ID No. 13
SEQ ID No. 7
SEQ ID No. 14

FIGURE 10-2

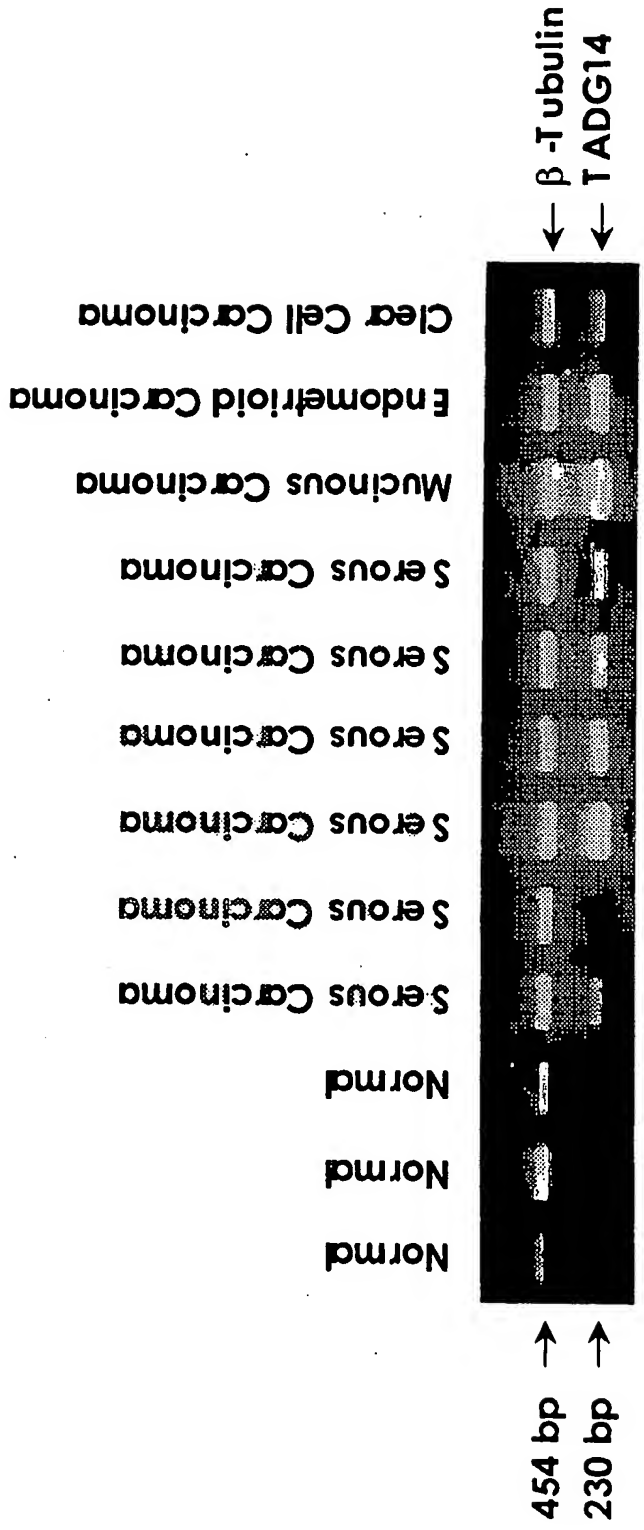
β-Tubulin
TADG14
Clear Cell Carcinoma
Endometrioid Carcinoma
Mucinous Carcinoma
Serous Carcinoma
Serous Carcinoma
Serous Carcinoma
Serous Carcinoma
Serous Carcinoma
Serous Carcinoma
Normal
Normal
Normal
454 bp
230 bp

FIGURE 11A

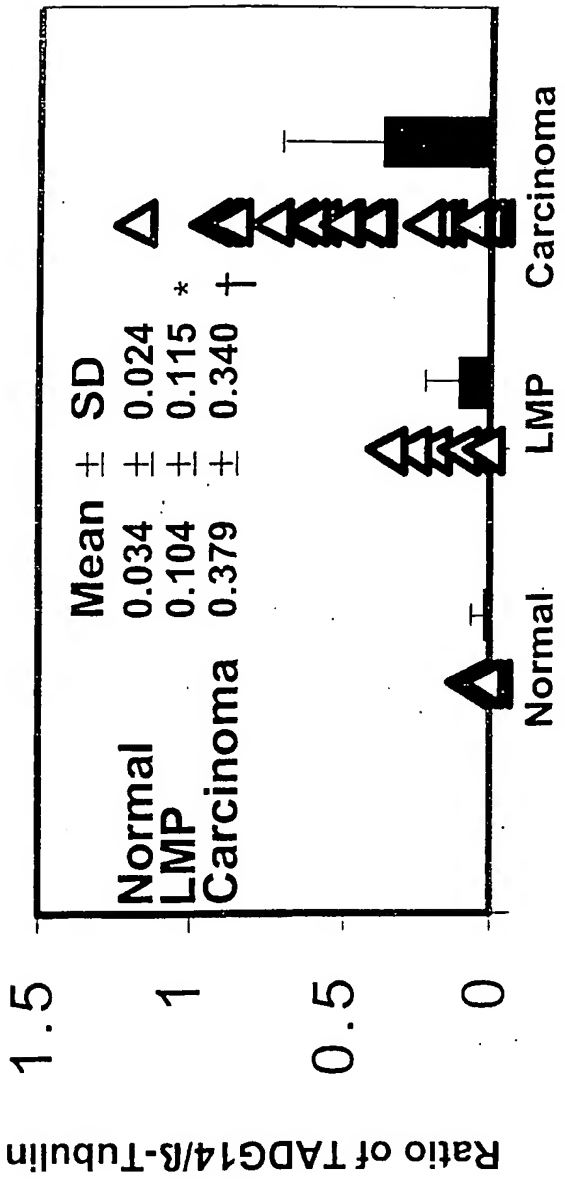
Ratio of TADG14/ß-Tubulin
1.5
1
0.5
0
Normal
LMP
Carcinoma
Normal
LMP
Carcinoma
Mean ± SD
0.034 ± 0.024
0.104 ± 0.115 *
0.379 ± 0.340 †

FIGURE 11B

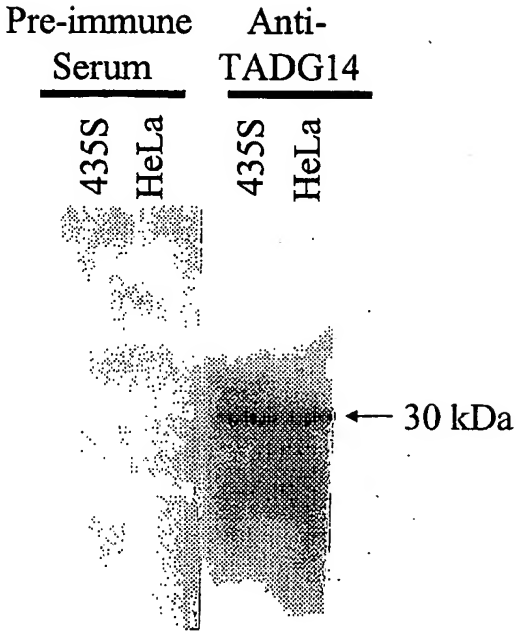

FIGURE 12

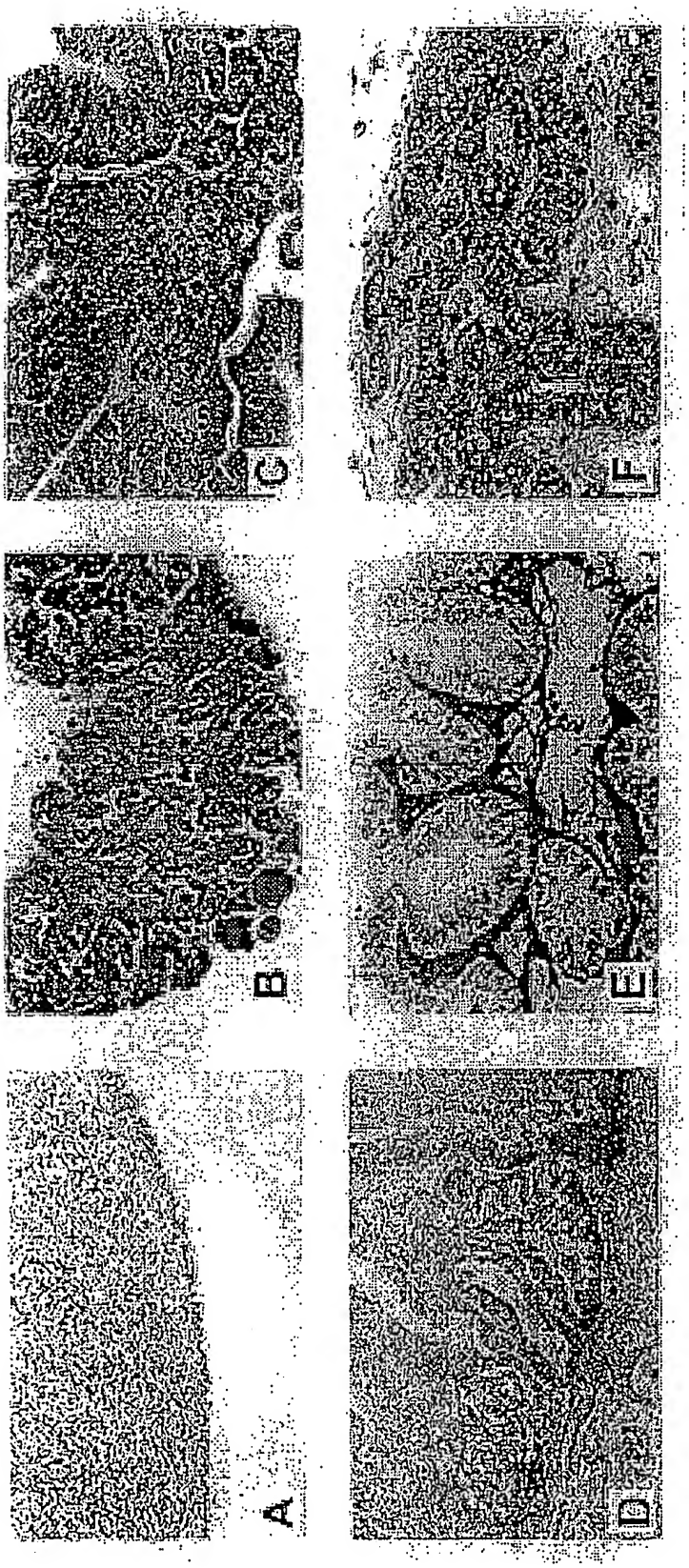

FIGURE 13

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/17372

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C12N 1/21, 5/10, 9/48, 9/50, 9/64, 15/55, 15/63
US CL :435/212, 219, 226, 252.3, 320.1, 325; 536/23.2

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/212, 219, 226, 252.3, 320.1, 325; 536/23.2

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, BIOSIS, MEDLINE, EMBASE
search terms: serine protease, ovarian cancer, neuropsin

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Chen, Z.-L. et al. Expression and Activity-Dependent Changes of a Novel Limbic-Serine Protease Gene in the Hippocampus. The Journal of Neuroscience. July 1995, Vol. 15, No. 7, pages 5088-5097, especially figure 1.	1, 4, 6-9, 11

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search 09 NOVEMBER 1998	Date of mailing of the international search report 19 NOV 1998
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer DIAN JACOBSON Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*